

WEST Search History

DATE: Tuesday, February 01, 2005

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L11	l10 and 392	2
<input type="checkbox"/>	L10	L9 and l6	9
<input type="checkbox"/>	L9	L8 and l5	13
<input type="checkbox"/>	L8	(530/387.1,387.7,388.1)![CCLS]	3884
<input type="checkbox"/>	L7	L6 and l5	139
<input type="checkbox"/>	L6	antibod\$.clm.	36182
<input type="checkbox"/>	L5	L4 or l3 or l1	13182
<input type="checkbox"/>	L4	algate.in.	25
<input type="checkbox"/>	L3	king.in.	13071
<input type="checkbox"/>	L2	king.in.L1	0
<input type="checkbox"/>	L1	Mitcham.in.	98

END OF SEARCH HISTORY

OM protein - protein search, using sw model

Run on: January 25, 2005, 11:36:37 ; Search time 157 Seconds
 (without alignments)
 706.034 Million cell updates/sec

Title: US-09-827-271-392
 Perfect score: 1574
 Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYMLK 309

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1574	100.0	309	3	AAB12556	Aab12556 Human ova
2	1574	100.0	309	4	AAB99205	Aab99205 Human ova
3	1574	100.0	309	5	ABP30900	Abp30900 O8E prote
4	1574	100.0	309	7	ADA08545	Ada08545 Human ova
5	1574	100.0	309	7	ADF08888	Adf08888 Secreted
6	1574	100.0	309	7	ADG46175	Adg46175 Human ova
7	1574	100.0	309	8	ADN40454	Adn40454 Human bre
8	1538	97.7	306	8	ADH50895	Adh50895 Breast an
9	1513	96.1	336	8	ADH50894	Adh50894 Breast an

10	1431	90.9	282	3	AAy66719	Aay66719	Membrane-
11	1431	90.9	282	3	AAB12557	Aab12557	Human ova
12	1431	90.9	282	4	AAU29132	Aau29132	Human PRO
13	1431	90.9	282	4	AAB87555	Aab87555	Human PRO
14	1431	90.9	282	4	AAB99204	Aab99204	Human ova
15	1431	90.9	282	4	AAB65242	Aab65242	Human PRO
16	1431	90.9	282	5	AAE20311	Aae20311	Human B7-
17	1431	90.9	282	5	ABG96445	Abg96445	Human ova
18	1431	90.9	282	5	AAU77766	Aau77766	Tumour as
19	1431	90.9	282	5	ABG95880	Abg95880	Human sec
20	1431	90.9	282	5	AAU76536	Aau76536	Tumour-as
21	1431	90.9	282	5	ABP30901	Abp30901	O8E prote
22	1431	90.9	282	5	ABB76274	Abb76274	Breast BS
23	1431	90.9	282	5	AAE18336	Aae18336	Human B7-
24	1431	90.9	282	5	ABB09879	Abb09879	Amino aci
25	1431	90.9	282	5	AAE19013	Aae19013	Human B7-
26	1431	90.9	282	6	ABU58508	Abu58508	Human PRO
27	1431	90.9	282	6	ABU88056	Abu88056	Novel hum
28	1431	90.9	282	6	ABU84371	Abu84371	Human sec
29	1431	90.9	282	6	ABR66245	Abr66245	Human sec
30	1431	90.9	282	6	ABR65635	Abr65635	Human sec
31	1431	90.9	282	6	ABU99575	Abu99575	Human sec
32	1431	90.9	282	6	ABU58057	Abu58057	Human PRO
33	1431	90.9	282	6	ABU59135	Abu59135	Novel hum
34	1431	90.9	282	6	ABU82647	Abu82647	Human sec
35	1431	90.9	282	6	ABU82814	Abu82814	Human PRO
36	1431	90.9	282	6	ABU89935	Abu89935	Novel hum
37	1431	90.9	282	6	ABR68184	Abr68184	Human sec
38	1431	90.9	282	6	ABU60566	Abu60566	Human sec
39	1431	90.9	282	6	ABU96237	Abu96237	Novel hum
40	1431	90.9	282	6	ABU92668	Abu92668	Human sec
41	1431	90.9	282	6	ABO08745	Abo08745	Human sec
42	1431	90.9	282	6	ABO02797	Abo02797	Human sec
43	1431	90.9	282	6	ABR74951	Abr74951	Human sec
44	1431	90.9	282	6	ABR94713	Abr94713	Human sec
45	1431	90.9	282	6	ABU13948	Abu13948	Human PRO

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 27, 2005, 13:05:30 ; Search time 4800 Seconds
(without alignments)
3044.274 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYMLK 309

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool_h/US09827271/runat_25012005_101614_10300/app_query.fasta_1
.455

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09827271_@CGN_1_1_3731_@runat_25012005_101614_10300 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1574	100.0	2627	6	BD265002	BD265002 Compositi
	2	1574	100.0	2627	6	AR238405	AR238405 Sequence
	3	1574	100.0	2627	6	AR478744	AR478744 Sequence
	4	1574	100.0	2627	6	AX156350	AX156350 Sequence
	5	1574	100.0	2627	6	AX366624	AX366624 Sequence
	6	1541	97.9	1065	6	AX375858	AX375858 Sequence
	7	1541	97.9	1965	6	CQ412191	CQ412191 Sequence
	8	1538	97.7	1070	9	AY346100	AY346100 Homo sapi
	9	1538	97.7	1658	6	AR252569	AR252569 Sequence
	10	1538	97.7	1658	6	AX092328	AX092328 Sequence
	11	1538	97.7	1658	6	AX376150	AX376150 Sequence
	12	1538	97.7	1658	6	AX395215	AX395215 Sequence
	13	1538	97.7	1658	6	AX403403	AX403403 Sequence
	14	1538	97.7	1658	6	AX468680	AX468680 Sequence
	15	1538	97.7	1658	9	AY358352	AY358352 Homo sapi
	16	1538	97.7	2626	6	AX375860	AX375860 Sequence
	17	1532	97.3	1811	9	AK026071	AK026071 Homo sapi
	18	1525	96.9	2587	6	BD235830	BD235830 A novel m
	19	1522	96.7	2603	6	AX403048	AX403048 Sequence
	20	1513	96.1	1190	9	BC065717	BC065717 Homo sapi
	21	1488	94.5	916	9	BC074729	BC074729 Homo sapi
	22	1431	90.9	849	9	AY280972	AY280972 Homo sapi
	23	1388.5	88.2	2671	9	HSM808167	BX648021 Homo sapi
	24	1266	80.4	1382	10	AY346099	AY346099 Mus muscu
	25	1261.5	80.1	852	10	AY322147	AY322147 Mus muscu
	26	1257.5	79.9	852	10	AY280973	AY280973 Mus muscu
	27	1257	79.9	1343	10	BC032925	BC032925 Mus muscu
	28	1202	76.4	94664	9	HSJ1025A1	AL080312 Human DNA
	29	1066	67.7	6370	6	AX403051	AX403051 Sequence
	30	812	51.6	548	6	CQ100653	CQ100653 Sequence
	31	812	51.6	548	6	CQ139644	CQ139644 Sequence
	32	812	51.6	548	6	CQ223013	CQ223013 Sequence
	33	812	51.6	548	6	CQ260975	CQ260975 Sequence
	34	812	51.6	548	6	CQ335117	CQ335117 Sequence
	35	777	49.4	462	6	BD235842	BD235842 A novel m
	36	759	48.2	456	6	AX182037	AX182037 Sequence
	37	690	43.8	513	6	CQ735047	CQ735047 Sequence
	38	638	40.5	406	6	BD235841	BD235841 A novel m
	39	610.5	38.8	390	6	AX098101	AX098101 Sequence
c	40	603	38.3	171595	9	AL391476	AL391476 Human DNA
	41	571	36.3	336	6	AX375856	AX375856 Sequence
	42	540.5	34.3	218776	2	AC134291	AC134291 Rattus no
c	43	540.5	34.3	286029	2	AC110845	AC110845 Rattus no

44	535.5	34.0	199673	10	AL669872
45	512	32.5	1463	5	BC044000

AL669872 Mouse DNA
BC044000 Xenopus l

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 27, 2005, 12:58:11 ; Search time 552 Seconds
(without alignments)
2938.535 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMLK 309

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool_h/US09827271/runat_25012005_101614_10291/app_query.fasta_1
.455

-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09827271_@CGN_1_1_470_@runat_25012005_101614_10291 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1574	100.0	2627	3	AAA70077	Aaa70077 Human ova
2	1574	100.0	2627	4	AAH55681	Aah55681 Human ova
3	1574	100.0	2627	6	ABN72971	Abn72971 Ovarian c
4	1574	100.0	2627	9	ADA08544	Ada08544 Human ova
5	1574	100.0	2627	10	ADF08887	Adf08887 cDNA enco
6	1574	100.0	2627	10	ADG46174	Adg46174 Human ova
7	1574	100.0	2627	12	ADN40452	Adn40452 Human bre
8	1541	97.9	1065	6	ABL56580	Abl56580 Nucleotid
9	1541	97.9	1965	5	ADL45372	Adl45372 Human ova
10	1538	97.7	1657	3	AAZ65059	Aaz65059 Membrane-
11	1538	97.7	1658	4	AAS46033	Aas46033 Human DNA
12	1538	97.7	1658	4	AAF92087	Aaf92087 Human PRO
13	1538	97.7	1658	5	AAF44205	Aaf44205 Human PRO
14	1538	97.7	1658	6	ABK11744	Abk11744 DNA encod
15	1538	97.7	1658	6	ABS74407	Abs74407 Human cDN
16	1538	97.7	1658	6	ABK11091	Abk11091 cDNA enco
17	1538	97.7	1658	8	ACA89483	Aca89483 cDNA enco
18	1538	97.7	1658	8	ACA73493	Aca73493 Human sec
19	1538	97.7	1658	8	ACA05808	Aca05808 Human sec
20	1538	97.7	1658	8	ACA66642	Aca66642 cDNA enco
21	1538	97.7	1658	8	ACA64352	Aca64352 Novel hum
22	1538	97.7	1658	8	ACA91193	Aca91193 Novel hum
23	1538	97.7	1658	8	ACD81570	Acd81570 Human cDN
24	1538	97.7	1658	8	ACF20217	Acf20217 Human sec
25	1538	97.7	1658	8	ACF19603	Acf19603 Human sec
26	1538	97.7	1658	8	ACD21891	Acd21891 Human sec
27	1538	97.7	1658	8	ACF13056	Acf13056 Human sec
28	1538	97.7	1658	8	ACD25159	Acd25159 Human sec
29	1538	97.7	1658	8	ACF00208	Acf00208 Human sec
30	1538	97.7	1658	8	ACA60392	Aca60392 Novel hum
31	1538	97.7	1658	8	ACA72265	Aca72265 Novel hum
32	1538	97.7	1658	8	ACD04789	Acd04789 Novel hum
33	1538	97.7	1658	8	ACD18250	Acd18250 Human sec
34	1538	97.7	1658	8	ACD08257	Acd08257 Human sec
35	1538	97.7	1658	8	ACA88691	Aca88691 Novel hum
36	1538	97.7	1658	8	ACA70133	Aca70133 Human sec
37	1538	97.7	1658	8	ACD12355	Acd12355 Novel hum
38	1538	97.7	1658	8	ACC74270	Acc74270 Human sec
39	1538	97.7	1658	8	ACD15898	Acd15898 Human sec
40	1538	97.7	1658	8	ACD25466	Acd25466 Novel hum
41	1538	97.7	1658	8	ACD17943	Acd17943 Human sec
42	1538	97.7	1658	8	ACC88230	Acc88230 Human sec
43	1538	97.7	1658	8	ACD21584	Acd21584 Human sec
44	1538	97.7	1658	8	ACD18651	Acd18651 Human sec
45	1538	97.7	1658	8	ACA58839	Aca58839 cDNA enco

OM protein - protein search, using sw model

Run on: January 25, 2005, 11:45:57 ; Search time 41 Seconds
(without alignments)
725.146 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYMLK 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	219.5	13.9	526	2	A37821	butyrophilin - bov
2	211.5	13.4	526	2	S70587	butyrophilin precu
3	171.5	10.9	487	2	S65133	butyrophilin - mou
4	168.5	10.7	391	2	T09058	butyrophilin homol
5	163.5	10.4	299	2	I46690	CD80 precursor - r
6	153	9.7	275	2	JC7604	CD86 spliced varia
7	151	9.6	339	2	T28138	Ig V-region-like B
8	150.5	9.6	340	2	T28137	Ig V-region-like B
9	150	9.5	247	2	A55717	myelin/oligodendro
10	147.5	9.4	329	1	A48754	B7-2 antigen - hum
11	147.5	9.4	330	2	I46691	CD86 precursor - r
12	147	9.3	218	2	B47712	myelin/oligodendro
13	146.5	9.3	372	2	C39371	Ig V-region-like B

14	146	9.3	398	2	A39371	Ig V-region-like B
15	144	9.1	247	2	S58394	myelin/oligodendro
16	143.5	9.1	309	2	I49522	gene B7-2 protein
17	140.5	8.9	246	2	A47712	myelin/oligodendro
18	135	8.6	761	1	IJHUNG	neural cell adhesi
19	134.5	8.5	503	2	JC5287	SHP substrate-1 pr
20	133	8.4	1091	1	IJCHNL	neural cell adhesi
21	132.5	8.4	853	1	IJBONC	neural cell adhesi
22	130.5	8.3	725	1	IJMSNG	neural cell adhesi
23	130.5	8.3	1033	2	S19247	cell adhesion prot
24	130.5	8.3	1115	1	IJMSNL	neural cell adhesi
25	128.5	8.2	858	1	IJRTNC	neural cell adhesi
26	127	8.1	946	1	A47299	ror-related recept
27	126.5	8.0	765	2	C42632	cell adhesion mole
28	126.5	8.0	812	2	B42632	cell adhesion mole
29	126.5	8.0	932	2	A42632	cell adhesion mole
30	126.5	8.0	1088	1	IJXLNL	neural cell adhesi
31	125.5	8.0	1018	2	JC4211	neural adhesion pr
32	124	7.9	309	2	I49503	B-lymphocyte activ
33	123.5	7.8	725	2	JE0099	neural cell adhesi
34	123.5	7.8	5175	2	T20992	hypothetical prote
35	123.5	7.8	5198	2	T43290	hemicentin precurs
36	122.5	7.8	871	1	I48696	protein-tyrosine k
37	122.5	7.8	881	1	I48697	protein-tyrosine k
38	121.5	7.7	1612	2	T30805	dutt1 protein - mo
39	121	7.7	321	2	I54766	B-lymphocyte activ
40	121	7.7	365	2	JC7780	coxsackie- and ade
41	121	7.7	1091	2	S01998	contactin precurs
42	120	7.6	215	2	A57843	sodium channel bet
43	120	7.6	288	2	A45803	B-cell-restricted
44	120	7.6	333	2	A31923	amalgam protein pr
45	118	7.5	321	2	D39371	Ig V-region-like B

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 27, 2005, 18:42:38 ; Search time 3530 Seconds
(without alignments)
3189.767 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYMLK 309

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool_h/US09827271/runat_25012005_101615_10326/app_query.fasta_1
.455
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09827271_@CGN_1_1_3437_@runat_25012005_101615_10326 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match %	Length	DB	ID	Description
	1	1288	81.8	2431	3	CR603772	CR603772 full-leng
	2	1184	75.2	714	7	CN259813	CN259813 170006000
	3	1087.5	69.1	757	4	BI454643	BI454643 603170538
	4	1046	66.5	767	5	BX358434	BX358434 BX358434
	5	1012	64.3	604	5	BX499180	BX499180 DKFZp779B
c	6	993	63.1	751	5	BM981657	BM981657 UI-CF-EN1
	7	931	59.1	702	6	BY736335	BY736335 BY736335
	8	889	56.5	578	6	CD686218	CD686218 EST2739 h
	9	889	56.5	655	7	CN259811	CN259811 170006000
	10	857.5	54.5	845	2	BF680206	BF680206 602154958
	11	847	53.8	670	2	BB666051	BB666051 BB666051
	12	838	53.2	925	5	BX369964	BX369964 BX369964
	13	834.5	53.0	917	2	BE573890	BE573890 601331875
	14	822	52.2	487	7	CN259818	CN259818 170006000
	15	802	51.0	639	2	BE381883	BE381883 601272421
c	16	752	47.8	595	5	BU680630	BU680630 UI-CF-DU1
	17	735	46.7	849	9	AY405846	AY405846 Homo sapi
	18	678	43.1	849	9	AY405847	AY405847 Pan trogl
	19	643.5	40.9	658	2	BE308473	BE308473 601090328
	20	632.5	40.2	852	9	AY405848	AY405848 Mus muscu
	21	624.5	39.7	487	1	AI155439	AI155439 ud85e11.r
	22	503.5	32.0	932	7	CR439118	CR439118 CR439118
c	23	489	31.1	443	1	AI799522	AI799522 tr49b02.x
	24	483	30.7	888	5	BQ734734	BQ734734 AGENCOURT
	25	480	30.5	847	6	CF223111	CF223111 AGENCOURT
	26	479.5	30.5	792	5	BU458718	BU458718 603367659
	27	476	30.2	830	4	BG172919	BG172919 602337353
	28	472	30.0	714	5	BX847707	BX847707 BX847707
c	29	470	29.9	436	8	AQ479831	AQ479831 RPCI-11-2
	30	462	29.4	292	1	AA333549	AA333549 EST37654
	31	423.5	26.9	712	5	BU471021	BU471021 603364509
	32	421	26.7	380	5	BY116902	BY116902 BY116902
	33	419	26.6	693	4	BJ043488	BJ043488 BJ043488
	34	418	26.6	882	6	CF238625	CF238625 AGENCOURT
	35	406	25.8	367	5	BY026217	BY026217 BY026217
	36	400	25.4	916	5	BQ731562	BQ731562 AGENCOURT
	37	387	24.6	679	4	BJ071648	BJ071648 BJ071648
	38	366	23.3	345	5	BY120095	BY120095 BY120095
	39	364	23.1	1141	3	CR729645	CR729645 Tetraodon
	40	362.5	23.0	608	1	AL676863	AL676863 AL676863
	41	358	22.7	341	5	BY117106	BY117106 BY117106
	42	357	22.7	1206	3	CR728324	CR728324 Tetraodon
	43	354	22.5	339	5	BY120008	BY120008 BY120008
	44	346	22.0	330	5	BY120640	BY120640 BY120640
	45	346	22.0	331	5	BY119734	BY119734 BY119734

OM protein - protein search, using sw model

Run on: January 25, 2005, 11:37:22 ; Search time 193 Seconds
 (without alignments)
 921.196 Million cell updates/sec

Title: US-09-827-271-392
 Perfect score: 1574
 Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYMLK 309

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1431	90.9	282	2	Q7Z7D3	Q7z7d3 homo sapien
2	1431	90.9	282	2	AAQ88718	Aaq88718 homo sapi
3	1431	90.9	282	2	AAQ24206	Aaq24206 homo sapi
4	1425	90.5	282	2	Q9H6B2	Q9h6b2 homo sapien
5	1261.5	80.1	283	2	Q7TPH5	Q7tph5 mus musculu
6	1257.5	79.9	283	2	Q7TSP5	Q7tsp5 mus musculu
7	1257.5	79.9	283	2	AAQ24205	Aaq24205 mus muscu
8	1253.5	79.6	283	2	Q8K091	Q8k091 mus musculu
9	958	60.9	187	2	Q6P097	Q6p097 homo sapien
10	958	60.9	187	2	AAH65717	Aah65717 homo sapi
11	512	32.5	285	2	Q7ZY30	Q7zy30 xenopus lae
12	448	28.5	275	2	Q8AVV1	Q8avv1 xenopus lae
13	255.5	16.2	305	2	Q6DJ75	Q6dj75 xenopus tro
14	247	15.7	316	2	Q9BXR1	Q9bxr1 homo sapien
15	246	15.6	388	2	Q8NC34	Q8nc34 homo sapien

16	246	15.6	493	2	Q6P5Y4	Q6p5y4 homo sapien
17	246	15.6	493	2	AAH62581	Aah62581 homo sapi
18	246	15.6	533	2	Q8NCB6	Q8ncb6 homo sapien
19	246	15.6	534	2	Q8NBI8	Q8nbi8 homo sapien
20	241	15.3	316	2	Q6UXI2	Q6uxi2 homo sapien
21	241	15.3	316	2	AAQ88709	Aaq88709 homo sapi
22	235	14.9	316	2	Q8VE98	Q8ve98 mus musculu
23	235	14.9	316	2	AAH56608	Aah56608 mus muscu
24	232	14.7	316	2	Q7TPB4	Q7tpb4 rattus norv
25	225.5	14.3	466	2	Q6UXE8	Q6uxe8 homo sapien
26	225.5	14.3	466	2	AAQ88751	Aaq88751 homo sapi
27	225	14.3	220	2	Q9NWQ6	Q9nwq6 homo sapien
28	225	14.3	414	2	Q9UM44	Q9um44 homo sapien
29	223	14.2	495	2	Q9HCY1	Q9hcy1 homo sapien
30	223	14.2	513	2	O00481	O00481 homo sapien
31	222.5	14.1	347	2	Q9H730	Q9h730 homo sapien
32	222.5	14.1	500	2	Q6UX41	Q6ux41 homo sapien
33	222.5	14.1	500	2	AAQ88887	Aaq88887 homo sapi
34	220	14.0	280	2	O73716	O73716 grus americ
35	219.5	13.9	286	2	O46535	O46535 bos taurus
36	215.5	13.7	304	2	Q9BE26	Q9be26 macaca fasc
37	215.5	13.7	526	1	BUTY_BOVIN	P18892 bos taurus
38	215.5	13.7	731	2	P78409	P78409 homo sapien
39	213.5	13.6	584	2	O00478	O00478 homo sapien
40	211.5	13.4	526	1	BUTY_HUMAN	Q13410 homo sapien
41	209.5	13.3	526	2	Q9H458	Q9h458 homo sapien
42	208.5	13.2	334	2	Q9NR44	Q9nr44 homo sapien
43	207.5	13.2	319	2	O00477	O00477 homo sapien
44	207.5	13.2	332	2	Q9BU81	Q9bu81 homo sapien
45	207.5	13.2	332	2	AAH02832	Aah02832 homo sapi

OM protein - protein search, using sw model

Run on: January 25, 2005, 11:45:17 ; Search time 40 Seconds
 (without alignments)
 512.307 Million cell updates/sec

Title: US-09-827-271-392
 Perfect score: 1574
 Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYMLK 309

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1574	100.0	309	4	US-09-404-879A-392	Sequence 392, App
2	1574	100.0	309	4	US-09-667-857-392	Sequence 392, App
3	1431	90.9	282	4	US-09-404-879A-393	Sequence 393, App
4	1431	90.9	282	4	US-09-667-857-393	Sequence 393, App
5	348	22.1	65	4	US-09-667-857-415	Sequence 415, App
6	247	15.7	316	4	US-09-910-174B-24	Sequence 24, Appl
7	247	15.7	316	4	US-09-620-461-24	Sequence 24, Appl
8	246	15.6	441	4	US-09-651-200-4	Sequence 4, Appli
9	246	15.6	534	4	US-09-651-200-6	Sequence 6, Appli
10	246	15.6	534	4	US-09-651-200-24	Sequence 24, Appl
11	245	15.6	340	4	US-09-651-200-2	Sequence 2, Appli

12	238.5	15.2	315	4	US-09-910-174B-28	Sequence 28, Appl
13	238.5	15.2	315	4	US-09-620-461-28	Sequence 28, Appl
14	223	14.2	513	4	US-09-910-174B-18	Sequence 18, Appl
15	223	14.2	513	4	US-09-620-461-18	Sequence 18, Appl
16	217.5	13.8	540	2	US-08-724-394A-4	Sequence 4, Appli
17	215.5	13.7	731	4	US-09-910-174B-15	Sequence 15, Appl
18	215.5	13.7	731	4	US-09-620-461-15	Sequence 15, Appl
19	213.5	13.6	584	4	US-09-910-174B-16	Sequence 16, Appl
20	213.5	13.6	584	4	US-09-620-461-16	Sequence 16, Appl
21	212.5	13.5	610	2	US-08-724-394A-5	Sequence 5, Appli
22	211.5	13.4	526	4	US-09-910-174B-9	Sequence 9, Appli
23	211.5	13.4	526	4	US-09-620-461-9	Sequence 9, Appli
24	211.5	13.4	589	2	US-08-724-394A-1	Sequence 1, Appli
25	207.5	13.2	319	4	US-09-910-174B-12	Sequence 12, Appl
26	207.5	13.2	319	4	US-09-620-461-12	Sequence 12, Appl
27	207.5	13.2	342	2	US-08-724-394A-6	Sequence 6, Appli
28	207.5	13.2	357	4	US-09-910-174B-14	Sequence 14, Appl
29	207.5	13.2	357	4	US-09-620-461-14	Sequence 14, Appl
30	204	13.0	290	4	US-09-910-174B-19	Sequence 19, Appl
31	204	13.0	290	4	US-09-620-461-19	Sequence 19, Appl
32	204	13.0	350	4	US-09-651-200-25	Sequence 25, Appl
33	204	13.0	350	4	US-09-910-174B-17	Sequence 17, Appl
34	204	13.0	350	4	US-09-620-461-17	Sequence 17, Appl
35	199.5	12.7	290	4	US-09-910-174B-32	Sequence 32, Appl
36	196	12.5	296	4	US-09-667-135-36	Sequence 36, Appl
37	193	12.3	527	4	US-09-910-174B-10	Sequence 10, Appl
38	193	12.3	527	4	US-09-620-461-10	Sequence 10, Appl
39	192	12.2	329	4	US-09-651-200-18	Sequence 18, Appl
40	192	12.2	329	4	US-09-303-040-6	Sequence 6, Appli
41	188.5	12.0	290	4	US-09-910-174B-8	Sequence 8, Appli
42	188.5	12.0	290	4	US-09-620-461-8	Sequence 8, Appli
43	186	11.8	529	4	US-09-910-174B-13	Sequence 13, Appl
44	186	11.8	529	4	US-09-620-461-13	Sequence 13, Appl
45	186	11.8	581	2	US-08-724-394A-2	Sequence 2, Appli

OM protein - protein search, using sw model

Run on: January 25, 2005, 11:54:35 ; Search time 145 Seconds
(without alignments)
769.920 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYMLK 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1574	100.0	309	9	US-09-778-320-209	Sequence 209, App
2	1574	100.0	309	9	US-09-910-689-209	Sequence 209, App
3	1574	100.0	309	9	US-09-884-441-392	Sequence 392, App
4	1574	100.0	309	10	US-09-907-969-392	Sequence 392, App
5	1574	100.0	309	10	US-09-827-271-392	Sequence 392, App
6	1574	100.0	309	13	US-10-010-742-209	Sequence 209, App
7	1574	100.0	309	14	US-10-198-053-392	Sequence 392, App
8	1574	100.0	309	16	US-10-714-389-209	Sequence 209, App
9	1574	100.0	309	16	US-10-717-296-209	Sequence 209, App
10	1431	90.9	282	9	US-09-778-320-208	Sequence 208, App
11	1431	90.9	282	9	US-09-850-178-33	Sequence 33, Appl
12	1431	90.9	282	9	US-09-877-065-8	Sequence 8, Appli
13	1431	90.9	282	9	US-09-989-722-291	Sequence 291, App
14	1431	90.9	282	9	US-09-989-723-291	Sequence 291, App
15	1431	90.9	282	9	US-09-989-279-291	Sequence 291, App
16	1431	90.9	282	9	US-09-989-727-291	Sequence 291, App
17	1431	90.9	282	9	US-09-910-689-208	Sequence 208, App
18	1431	90.9	282	9	US-09-989-731-291	Sequence 291, App
19	1431	90.9	282	9	US-09-884-441-393	Sequence 393, App
20	1431	90.9	282	9	US-09-989-732-291	Sequence 291, App
21	1431	90.9	282	9	US-09-991-073-291	Sequence 291, App
22	1431	90.9	282	9	US-09-990-442-291	Sequence 291, App
23	1431	90.9	282	9	US-09-991-163-291	Sequence 291, App
24	1431	90.9	282	9	US-09-993-604-291	Sequence 291, App
25	1431	90.9	282	9	US-09-990-456-291	Sequence 291, App
26	1431	90.9	282	9	US-09-989-721-291	Sequence 291, App
27	1431	90.9	282	9	US-09-992-598-291	Sequence 291, App
28	1431	90.9	282	9	US-09-896-738-2	Sequence 2, Appli
29	1431	90.9	282	9	US-09-915-789A-5	Sequence 5, Appli
30	1431	90.9	282	9	US-09-989-293A-291	Sequence 291, App
31	1431	90.9	282	9	US-09-989-735-291	Sequence 291, App
32	1431	90.9	282	9	US-09-990-444-291	Sequence 291, App
33	1431	90.9	282	9	US-09-991-181-291	Sequence 291, App
34	1431	90.9	282	9	US-09-989-730-291	Sequence 291, App
35	1431	90.9	282	9	US-09-990-436-291	Sequence 291, App
36	1431	90.9	282	9	US-09-993-687-291	Sequence 291, App
37	1431	90.9	282	10	US-09-989-734-291	Sequence 291, App
38	1431	90.9	282	10	US-09-997-653-291	Sequence 291, App
39	1431	90.9	282	10	US-09-989-724-291	Sequence 291, App
40	1431	90.9	282	10	US-09-989-728-291	Sequence 291, App
41	1431	90.9	282	10	US-09-990-441-291	Sequence 291, App
42	1431	90.9	282	10	US-09-993-667-291	Sequence 291, App
43	1431	90.9	282	10	US-09-997-428-291	Sequence 291, App
44	1431	90.9	282	10	US-09-997-666-291	Sequence 291, App
45	1431	90.9	282	10	US-09-990-438-291	Sequence 291, App

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 27, 2005, 18:59:23 ; Search time 107 Seconds
(without alignments)
2052.652 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMLK 309

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool_h/US09827271/runat_25012005_101615_10354/app_query.fasta_1
.455

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09827271_@CGN_1_1_69_@runat_25012005_101615_10354 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1574	100.0	2627	4	US-09-404-879A-391	Sequence 391, App	
2	1574	100.0	2627	4	US-09-667-857-391	Sequence 391, App	
3	1379	87.6	1046	4	US-09-799-451-332	Sequence 332, App	
4	246	15.6	1323	4	US-09-651-200-9	Sequence 9, Appli	
5	246	15.6	1602	4	US-09-651-200-11	Sequence 11, Appl	
6	246	15.6	2229	4	US-09-651-200-5	Sequence 5, Appli	
7	246	15.6	2691	4	US-09-651-200-1	Sequence 1, Appli	
8	246	15.6	2885	4	US-09-651-200-3	Sequence 3, Appli	
9	246	15.6	3063	4	US-09-620-312D-844	Sequence 844, App	
10	245	15.6	1020	4	US-09-651-200-7	Sequence 7, Appli	
11	243	15.4	951	4	US-09-910-174B-23	Sequence 23, Appl	
12	243	15.4	951	4	US-09-620-461-23	Sequence 23, Appl	
13	238.5	15.2	948	4	US-09-910-174B-27	Sequence 27, Appl	
14	238.5	15.2	948	4	US-09-620-461-27	Sequence 27, Appl	
15	223	14.2	3416	2	US-08-724-394A-15	Sequence 15, Appl	
16	213.5	13.6	2926	2	US-08-724-394A-13	Sequence 13, Appl	
17	213.5	13.6	2970	4	US-09-566-921-105	Sequence 105, App	
18	209	13.3	1645	2	US-08-724-394A-14	Sequence 14, Appl	
19	199.5	12.7	1080	4	US-09-303-040-5	Sequence 5, Appli	
20	193	12.3	2882	2	US-08-724-394A-12	Sequence 12, Appl	
21	188.5	12.0	873	4	US-09-910-174B-22	Sequence 22, Appl	
22	188.5	12.0	873	4	US-09-620-461-22	Sequence 22, Appl	
23	183	11.6	3502	2	US-08-724-394A-16	Sequence 16, Appl	
24	163.5	10.4	900	4	US-09-495-052-61	Sequence 61, Appl	
25	160	10.2	3479	4	US-10-140-002-123	Sequence 123, App	
26	158	10.0	1163	3	US-08-479-744A-22	Sequence 22, Appl	
27	158	10.0	1163	3	US-08-280-757B-22	Sequence 22, Appl	
28	158	10.0	1163	4	US-09-425-762-22	Sequence 22, Appl	
29	157.5	10.0	1151	2	US-08-456-104-3	Sequence 3, Appli	
30	157.5	10.0	1151	3	US-08-205-697A-20	Sequence 20, Appl	
31	157.5	10.0	1151	3	US-08-702-525-20	Sequence 20, Appl	
32	157.5	10.0	1151	4	US-09-837-867A-20	Sequence 20, Appl	
33	157.5	10.0	1151	4	US-09-206-132-3	Sequence 3, Appli	
34	157.5	10.0	1151	5	PCT-US95-02576-20	Sequence 20, Appl	
35	157.5	10.0	1183	4	US-09-441-411-23	Sequence 23, Appl	
36	157.5	10.0	1261	3	US-08-205-697A-12	Sequence 12, Appl	
37	157.5	10.0	1261	3	US-08-702-525-12	Sequence 12, Appl	
38	157.5	10.0	1261	4	US-09-837-867A-12	Sequence 12, Appl	
39	157.5	10.0	1261	5	PCT-US95-02576-12	Sequence 12, Appl	
40	154	9.8	1424	3	US-09-326-186B-226	Sequence 226, App	
41	154	9.8	1424	4	US-09-441-411-21	Sequence 21, Appl	
42	154	9.8	1428	5	PCT-US94-09642-1	Sequence 1, Appli	
43	149.5	9.5	1161	3	US-08-205-697A-24	Sequence 24, Appl	
44	149.5	9.5	1161	3	US-08-702-525-24	Sequence 24, Appl	
45	149.5	9.5	1161	4	US-09-837-867A-24	Sequence 24, Appl	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 27, 2005, 21:14:25 ; Search time 624 Seconds
(without alignments)
2845.320 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09827271_@CGN_1_1_480_@runat_25012005_101618_10496
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	1574	100.0	2627	9	US-09-778-320-207	Sequence 207, App
2	1574	100.0	2627	9	US-09-910-689-207	Sequence 207, App
3	1574	100.0	2627	9	US-09-884-441-391	Sequence 391, App
4	1574	100.0	2627	10	US-09-907-969-391	Sequence 391, App
5	1574	100.0	2627	10	US-09-827-271-391	Sequence 391, App
6	1574	100.0	2627	13	US-10-010-742-207	Sequence 207, App
7	1574	100.0	2627	15	US-10-198-053-391	Sequence 391, App
8	1574	100.0	2627	17	US-10-714-389-207	Sequence 207, App
9	1574	100.0	2627	17	US-10-717-296-207	Sequence 207, App
10	1541	97.9	1065	9	US-09-877-065-5	Sequence 5, Appli
11	1541	97.9	1965	10	US-09-814-353-19262	Sequence 19262, A
12	1538	97.7	1658	9	US-09-989-722-290	Sequence 290, App
13	1538	97.7	1658	9	US-09-989-723-290	Sequence 290, App
14	1538	97.7	1658	9	US-09-989-279-290	Sequence 290, App
15	1538	97.7	1658	9	US-09-989-727-290	Sequence 290, App
16	1538	97.7	1658	9	US-09-989-731-290	Sequence 290, App
17	1538	97.7	1658	9	US-09-989-732-290	Sequence 290, App
18	1538	97.7	1658	9	US-09-991-073-290	Sequence 290, App
19	1538	97.7	1658	9	US-09-990-442-290	Sequence 290, App
20	1538	97.7	1658	9	US-09-991-163-290	Sequence 290, App
21	1538	97.7	1658	9	US-09-993-604-290	Sequence 290, App
22	1538	97.7	1658	9	US-09-990-456-290	Sequence 290, App
23	1538	97.7	1658	9	US-09-989-721-290	Sequence 290, App
24	1538	97.7	1658	9	US-09-992-598-290	Sequence 290, App
25	1538	97.7	1658	9	US-09-989-293A-290	Sequence 290, App
26	1538	97.7	1658	9	US-09-989-735-290	Sequence 290, App
27	1538	97.7	1658	9	US-09-990-444-290	Sequence 290, App
28	1538	97.7	1658	9	US-09-991-181-290	Sequence 290, App
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31	1538	97.7	1658	9	US-09-993-687-290	Sequence 290, App
32	1538	97.7	1658	10	US-09-989-734-290	Sequence 290, App
33	1538	97.7	1658	10	US-09-997-653-290	Sequence 290, App
34	1538	97.7	1658	10	US-09-989-724-290	Sequence 290, App
35	1538	97.7	1658	10	US-09-989-728-290	Sequence 290, App
36	1538	97.7	1658	10	US-09-990-441-290	Sequence 290, App

37	1538	97.7	1658	10	US-09-993-667-290	Sequence 290, App
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40	1538	97.7	1658	10	US-09-990-438-290	Sequence 290, App
41	1538	97.7	1658	10	US-09-990-562-290	Sequence 290, App
42	1538	97.7	1658	10	US-09-990-711-290	Sequence 290, App
43	1538	97.7	1658	10	US-09-989-726-290	Sequence 290, App
44	1538	97.7	1658	10	US-09-998-156-290	Sequence 290, App
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